

CLAIMS:

1. A method for assembling two or more DNA fragments with high efficiency, comprising:
 - a) providing, for each DNA fragment, at least one protruding terminus, or “overhang”, capable of hydrogen bonding to a complementary sequence on at least one strand of a second DNA fragment, said overhang and said complementary sequence having at least 15 bases; and
 - b) mixing two or more said DNA fragments under conditions suitable to promote joining thereof.
2. A method according to claim 1, wherein the number of fragments joined is three or more.
3. A method according to claim 1 or 2, wherein the overhang has at least 20 bases.
4. A method according to claim 1 or 2, wherein the number of bases in the overhang is between about 20 and about 30.
5. A method according to claim 2, wherein the molar ratio of each DNA pair is between about 1:1 and 1:50
6. A method according to any one of claims 1 to 5, essentially as described and with particular reference to the examples.
7. A DNA construct, whenever prepared by the method of any one of claims 1 to 5.
8. A DNA fragment comprising an overhang of at least 15 nucleotides or an end portion suitable to be converted into such an overhang.
9. A DNA fragment as claimed in claim 8, for use in the method of claim 1.